

RAW SEQUENCE LISTING

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Application Serial Number: 10/504,756

Source: PST

Date Processed by STIC: 1-9-05

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RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/10/501,756

TIME: 14:46:48

PCT

Input Set : D:\180-137 PCT.ST25.txt

Output Set: N:\CRF4\01042005\J501756.raw

A

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3 <110> APPLICANT: Duke University
4     Chuan-Yuan, Li
5     Xiuwu, Zhang
7 <120> TITLE OF INVENTION: GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY
A
8     COMPLETE ADENOVIRUS-MEDIATED APPROACH
10 <130> FILE REFERENCE: 180/137
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/501,756
C--> 12 <141> CURRENT FILING DATE: 2004-07-16
12 <150> PRIOR APPLICATION NUMBER: US 60/349,532
13 <151> PRIOR FILING DATE: 2002-01-18
15 <160> NUMBER OF SEQ ID NOS: 22
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1611
21 <212> TYPE: DNA
22 <213> ORGANISM: adeno-associated virus 2
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1611)
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32 1          5          10          15
34 gag cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag      96
35 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
36          20          25          30
38 aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att      144
39 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
40          35          40          45
42 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg      192
43 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
44          50          55          60
46 acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg      240
47 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
48 65          70          75          80
50 caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa      288
51 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
52          85          90          95
54 acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att      336
55 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
56          100          105          110
58 cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg      384
59 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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60	115	120	125	
62	cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg	432		
63	Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly			
64	130	135	140	
66	aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa	480		
67	Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys			
68	145	150	155	160
70	acc cag cct gag ctc cag tgg gcg tgg act aat atg gaa cag tat tta	528		
71	Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu			
72	165	170	175	
74	agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat	576		
75	Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His			
76	180	185	190	
78	ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat	624		
79	Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn			
80	195	200	205	
82	ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac	672		
83	Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr			
84	210	215	220	
86	atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag	720		
87	Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys			
88	225	230	235	240
90	cag tgg atc cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc	768		
91	Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala			
92	245	250	255	
94	tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag	816		
95	Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys			
96	260	265	270	
98	att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag	864		
99	Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln			
100	275	280	285	
102	ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta	912		
103	Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu			
104	290	295	300	
106	aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc	960		
107	Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala			
108	305	310	315	320
110	acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca	1008		
111	Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala			
112	325	330	335	
114	act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc	1056		
115	Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro			
116	340	345	350	
118	ttc tac ggg tgc gta aac tgg acc aat gag aac ttt ccc ttc aac gac	1104		
119	Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp			
120	355	360	365	
122	tgt gtc gac aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc	1152		
123	Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala			
124	370	375	380	

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126 aag gtc gtg gag tcg gcc aaa gcc att ctc gga gga agc aag gtg cgc      1200
127 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
128 385                               390                               395                               400
130 gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg      1248
131 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
132                               405                               410                               415
134 atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca      1296
135 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
136                               420                               425                               430
138 acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt      1344
139 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
140                               435                               440                               445
142 gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag      1392
143 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
144                               450                               455                               460
146 gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg      1440
147 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
148 465                               470                               475                               480
150 gag cat gaa ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc      1488
151 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
152                               485                               490                               495
154 ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt      1536
155 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
156                               500                               505                               510
158 gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac      1584
159 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
160                               515                               520                               525
162 aga ttg gct cga gga cac tct ctc tga      1611
163 Arg Leu Ala Arg Gly His Ser Leu
164                               530                               535
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 536
169 <212> TYPE: PRT
170 <213> ORGANISM: adeno-associated virus 2
172 <400> SEQUENCE: 2
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179                               20                               25                               30
182 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
183                               35                               40                               45
186 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
187                               50                               55                               60
190 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
191 65                               70                               75                               80
194 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
195                               85                               90                               95
198 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
199                               100                               105                               110

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202 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
203      115      120      125
206 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
207      130      135      140
210 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
211 145      150      155      160
214 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
215      165      170      175
218 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
219      180      185      190
222 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
223      195      200      205
226 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
227      210      215      220
230 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
231 225      230      235      240
234 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
235      245      250      255
238 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
239      260      265      270
242 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
243      275      280      285
246 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
247      290      295      300
250 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
251 305      310      315      320
254 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
255      325      330      335
258 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
259      340      345      350
262 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
263      355      360      365
266 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
267      370      375      380
270 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
271 385      390      395      400
274 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
275      405      410      415
278 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
279      420      425      430
282 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
283      435      440      445
286 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
287      450      455      460
290 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
291 465      470      475      480
294 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
295      485      490      495
298 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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299          500          505          510
302 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
303          515          520          525
306 Arg Leu Ala Arg Gly His Ser Leu
307          530          535
310 <210> SEQ ID NO: 3
311 <211> LENGTH: 1866
312 <212> TYPE: DNA
313 <213> ORGANISM: adeno-associated virus 2
316 <220> FEATURE:
317 <221> NAME/KEY: CDS
318 <222> LOCATION: (1)..(1866)
320 <400> SEQUENCE: 3
321 atg ccg ggg ttt tac gag att gtg att aag gtc ccc agc gac ctt gac      48
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323 1          5          10          15
325 ggg cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag      96
326 Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
327          20          25          30
329 aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att      144
330 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
331          35          40          45
333 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg      192
334 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
335          50          55          60
337 acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg      240
338 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
339 65          70          75          80
341 caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa      288
342 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
343          85          90          95
345 acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att      336
346 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
347          100          105          110
349 cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg      384
350 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
351          115          120          125
353 cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg      432
354 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
355          130          135          140
357 aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag      480
358 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
359 145          150          155          160
361 acc cag cct gaa ctg cag tgg gcg tgg act aat atg gaa cag tat tta      528
362 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
363          165          170          175
365 agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat      576
366 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
367          180          185          190

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VERIFICATION SUMMARY

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Input Set : D:\180-137 PCT.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date